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(54) Title: INFLAMMATION–ASSOCIATED GENES

(57) Abstract

The invention provides novel inflammation–associated genes and polypeptides encoded by those genes. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating or preventing diseases associated with inflammation.

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INFLAMMATION-ASSOCIATED GENES

TECHNICAL FIELD

The invention relates to 11 inflammation-associated genes identified by their coexpression with known inflammation genes; to their corresponding polypeptides: and to the use of these biomolecules in diagnosis, prognosis, prevention and evaluation of therapies for diseases associated with inflammation.

BACKGROUND ART

Inflammation is the body's immediate, general response to wounding or infection by a pathogen. There are many complex phenomena that occur during an inflammation response. Initiation of the complement cascade, leukocyte recruitment, and leukocyte activation are three key events. In the complement cascade, a set of serum proteins, collectively called complement, non-specifically coat foreign matter. The coating proceeds in a cascade of steps using particular subsets of factors called complement components. The coated particles are then phagocytosed by macrophages or neutrophils recruited to the inflammation site. Leukocyte recruitment of monocytes and neutrophils is mediated by cytokines, which are proteins secreted by tissue at the inflammation site. Interleukin-8 (IL-8) is the primary chemoattractant cytokine responsible for recruitment in the initial stage of inflammation. In response to IL-8, monocytes and neutrophils are activated. An immediate response to activation is the expression of L-selectin and the integrins. L-selectin is a surface molecule that facilitates leukocyte binding (with relatively low affinity) to the endothelial cells lining blood vessels in the vicinity of the inflammation site. The integrins, also cell surface molecules, have stronger binding and mediate the actual extravasation of leukoctyes from the blood vessel. Upon reaching the site of inflammation, receptors to the complement factors coating foreign particles are expressed on the leukocytes leading to phagocytosis and enzymatic degradation. Many genes that participate in and regulate the inflammation response are known, but many remain to be identified. Identification of currently unknown genes will provide new diagnostic and therapeutic targets for control of the inflammation response and treatment of inflammatory disorders.

The present invention provides new compositions that are useful for control of inflammation and for the diagnosis, prognosis, treatment, prevention, and evaluation of therapies for inflammatory disorders such as rheumatoid arthritis, Crohn's disease, multiple sclerosis, asthma and allergy. We have identified 11 novel inflammation-associated genes by their coexpression with known inflammation genes.

DISCLOSURE OF THE INVENTION

In one aspect, the invention provides for a substantially purified polynucleotide comprising a gene that is coexpressed with one or more known inflammation genes in a plurality of biological samples. Preferably, known inflammation genes are selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits p67phox, p47phox, and p40phox, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase. Preferred embodiments include (a) a polynucleotide sequence of SEQ ID NOs:1-11; (b) a polynucleotide sequence which encodes the polypeptide sequence 12, 13, 14, 15, 16, or 17; (c) a polynucleotide sequence having at least 70% identity to the polynucleotide sequence of (a) or (b); (d) a polynucleotide sequence which is complementary to the polynucleotide sequence of (a), (b), or (c); (e) a polynucleotide sequence comprising at least 10, preferably at least 18, sequential nucleotides of the polynucleotide sequence of (a), (b), (c), or (d); and (f) a polynucleotide which hybridizes under stringent conditions to the polynucleotide of (a), (b), (c), (d) or (e). Furthermore, the invention provides an expression vector comprising any of the above described polynucleotides and host cells comprising the expression vector. Still further, the invention provides a method for treating or preventing a disease or condition associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes comprising administering to a subject in need a polynucleotide described above in an amount effective for treating or preventing said disease.

In a second aspect, the invention provides a substantially purified polypeptide comprising the gene product of a gene that is coexpressed with one or more known inflammation genes in a plurality of biological samples. The known inflammation gene may be selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits p67phox, p47phox, and p40phox, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase. Preferred embodiments are (a) the polypeptide sequence of SEQ ID NOs:12, 13, 14, 15, 16, or 17; (b) a polypeptide sequence having at least 85% identity to the polypeptide sequence of (a); and (c) a polypeptide sequence comprising at least 6 sequential amino acids of the polypeptide sequence of (a) or (b). Additionally, the invention provides antibodies that bind specifically to any of the above described polypeptides and a method for treating or preventing a disease or condition associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes comprising administering to a subject in need such an antibody in an amount effective for treating or preventing said disease.

In another aspect, the invention provides a pharmaceutical composition comprising the polynucleotide or the polypeptide in conjunction with a suitable pharmaceutical carrier and a

method for treating or preventing a disease or condition associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes comprising administering to a subject in need such a composition in an amount effective for treating or preventing said disease.

In a further aspect, the invention provides a ribozyme that cleaves a polynucleotide of the invention and a method for treating or preventing a disease or condition associated with the increased expression of a gene that is coexpressed with one or more known inflammation genes. The method comprises administering to a subject in need the ribozyme in an amount effective for treating or preventing the disease.

In yet a further aspect, the invention provides a method for diagnosing a disease or condition associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits p67phox, p47phox, and p40phox, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase. The method comprises the steps of (a) providing the sample comprising one of more of said coexpressed genes; (b) hybridizing the polynucleotide to said coexpressed genes under conditions effective to form one or more hybridization complexes; (c) detecting the hybridization complexes; and (d) comparing the levels of the hybridization complexes with the level of hybridization complexes in a nondiseased sample, wherein altered levels of one or more of the hybridization complexes in a diseased sample compared with the level of hybridization complexes in a non-diseased sample correlates with the presence of the disease or condition.

Additionally, the invention provides antibodies that bind specifically to any of the above described polypeptides and a method for treating or preventing a disease or condition associated with the inflammation response.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

The Sequence Listing provides exemplary inflammation-associated sequences including polynucleotide sequences, SEQ ID NOs:1-11, and polypeptide sequences, SEQ ID NOs:12-17. Each sequence is identified by a sequence identification number (SEQ ID NO) and by the Incyte Clone number from which the sequence was first identified.

DESCRIPTION OF THE INVENTION

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include the plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those

skilled in the art, and so forth.

DEFINITIONS

"NSEQ" refers generally to a polynucleotide sequence of the present invention including SEQ ID NOs:1-11. "PSEQ" refers generally to a polypeptide sequence of the present invention including SEQ ID NOs:12-17.

A " variant" refers to either a polynucleotide or a polypeptide whose sequence diverges from SEQ ID NOs:1-11 or SEQ ID NOs:12-17, respectively. Polynucleotide sequence divergence may result from mutational changes such as deletions, additions, and substitutions of one or more nucleotides; it may also occur because of differences in codon usage. Each of these types of changes may occur alone, or in combination, one or more times in a given sequence. Polypeptide variants include sequences that possess at least one structural or functional characteristic of SEQ ID NOs:12-17.

A "fragment" can refer to a nucleic acid sequence that is preferably at least 20 nucleic acids in length, more preferably 40 nucleic acids, and most preferably 60 nucleic acids in length, and encompasses, for example, fragments consisting of nucleic acids 1-50 of SEQ ID NOs:1-11. A "fragment" can also refer to polypeptide sequences which are preferably at least 5 to about 15 amino acids in length, most preferably at least 10 amino acids, and which retain some biological or immunological activity of, for example, a sequence selected from SEQ ID NOs:12-17.

"Gene" or "gene sequence" refers to the partial or complete coding sequence of a gene. The term also refers to 5' or 3' untranslated regions. The gene may be in a sense or antisense (complementary) orientation.

"Known inflammation gene" refers to a gene sequence which has been previously identified as useful in the diagnosis, treatment, prognosis, or prevention of diseases associated with inflammation. Typically, this means that the known gene is expressed at higher levels in tissue abundant in known inflammation transcripts when compared with other tissue.

"Inflammation-associated gene" refers to a gene sequence whose expression pattern is similar to that of the known inflammation genes and which are useful in the diagnosis, treatment, prognosis, or prevention of diseases associated with inflammation, particularly disorders such as rheumatoid arthritis, Crohn's disease, multiple sclerosis, asthma and allergy.

"Substantially purified" refers to a nucleic acid or an amino acid sequence that is removed from its natural environment and is isolated or separated, and is at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which it is naturally present.

THE INVENTION

The present invention encompasses a method for identifying biomolecules that are associated with a specific disease, regulatory pathway, subcellular compartment, cell type, tissue type, or species. In particular, the method identifies gene sequences useful in diagnosis, prognosis, treatment, prevention, and evaluation of therapies for diseases associated with inflammation, particularly disorders such as rheumatoid arthritis, Crohn's disease, multiple sclerosis, asthma and allergy.

The method entails first identifying polynucleotides that are expressed in a plurality cDNA libraries. The identified polynucleotides include genes of known function, genes known to be specifically expressed in a specific disease process, subcellular compartment, cell type, tissue type, or species. Additionally, the polynucleotides include genes of unknown function. The expression patterns of the known genes are then compared with those of the genes of unknown function to determine whether a specified coexpression probability threshold is met. Through this comparison, a subset of the polynucleotides having a high coexpression probability with the known genes can be identified. The high coexpression probability correlates with a particular coexpression probability threshold which is less than 0.001, and more preferably less than 0.00001.

The polynucleotides originate from cDNA libraries derived from a variety of sources including, but not limited to, eukaryotes such as human, mouse, rat, dog, monkey, plant, and yeast and prokaryotes such as bacteria and viruses. These polynucleotides can also be selected from a variety of sequence types including, but not limited to, expressed sequence tags (ESTs), assembled polynucleotide sequences, full length gene coding regions, introns, regulatory sequences, 5' untranslated regions, and 3' untranslated regions. To have statistically significant analytical results, the polynucleotides need to be expressed in at least three cDNA libraries.

The cDNA libraries used in the coexpression analysis of the present invention can be obtained from blood vessels, heart, blood cells, cultured cells, connective tissue, epithelium, islets of Langerhans, neurons, phagocytes, biliary tract, esophagus, gastrointestinal system, liver, pancreas, fetus, placenta, chromaffin system, endocrine glands, ovary, uterus, penis, prostate, seminal vesicles, testis, bone marrow, immune system, cartilage, muscles, skeleton, central nervous system, ganglia, neuroglia, neurosecretory system, peripheral nervous system, bronchus, larynx, lung, nose, pleurus, ear, eye, mouth, pharynx, exocrine glands, bladder, kidney, ureter, and the like. The number of cDNA libraries selected can range from as few as 3 to greater than 10,000. Preferably, the number of the cDNA libraries is greater than 500.

In a preferred embodiment, gene sequences are assembled to reflect related sequences,

such as assembled sequence fragments derived from a single transcript. Assembly of the polynucleotide sequences can be performed using sequences of various types including, but not limited to, ESTs, extensions, or shotgun sequences. In a most preferred embodiment, the polynucleotide sequences are derived from human sequences that have been assembled using the algorithm disclosed in "Database and System for Storing, Comparing and Displaying Related Biomolecular Sequence Information", Lincoln et al., Serial No:60/079,469, filed March 26, 1998, incorporated herein by reference.

Experimentally, differential expression of the polynucleotides can be evaluated by methods including, but not limited to, differential display by spatial immobilization or by gel electrophoresis, genome mismatch scanning, representational difference analysis, and transcript imaging. Additionally, differential expression can be assessed by microarray technology. These methods may be used alone or in combination.

Known inflammation genes can be selected based on the use of the genes as diagnostic or prognostic markers or as therapeutic targets for diseases associated with inflammation. Preferably, the known inflammation genes include CD16, L-selectin, Src-like adapter protein (SLAP), IP-30, superoxidase homoenzyme subunits (p67phox, p47phox, and p40phox), alpha-1-antitrypsin (AAT), Clq-A, 5-lipoxygenase activating protein (FLAP), and SRC family tyrosine kinase (HCK), and the like.

The procedure for identifying novel genes that exhibit a statistically significant coexpression pattern with known inflammation genes is as follows. First, the presence or absence of a gene sequence in a cDNA library is defined: a gene is present in a cDNA library when at least one cDNA fragment corresponding to that gene is detected in a cDNA sample taken from the library, and a gene is absent from a library when no corresponding cDNA fragment is detected in the sample.

Second, the significance of gene coexpression is evaluated using a probability method to measure a due-to-chance probability of the coexpression. The probability method can be the Fisher exact test, the chi-squared test, or the kappa test. These tests and examples of their applications are well known in the art and can be found in standard statistics texts (Agresti (1990) Categorical Data Analysis, John Wiley $ Sons, New York NY; Rice (1988) Mathematical Statistics and Data Analysis, Duxbury Press, Pacific Grove CA). A Bonferroni correction (Rice, supra, page 384) can also be applied in combination with one of the probability methods for correcting statistical results of one gene versus multiple other genes. In a preferred embodiment, the due-to-chance probability is measured by a Fisher exact test, and the threshold of the due-to-chance probability is set to less than 0.001, more preferably less than 0.00001.

To determine whether two genes, A and B, have similar coexpression patterns, occurrence data vectors can be generated as illustrated in Table 1, wherein a gene's presence is indicated by a one and its absence by a zero. A zero indicates that the gene did not occur in the library, and a one indicates that it occurred at least once.

Table 1. Occurrence data for genes A and B

	Library 1	Library 2	Library 3	...	Library N
gene A	1	1	0	...	0
gene B	1	0	1	...	0

For a given pair of genes, the occurrence data in Table 1 can be summarized in a 2 x 2 contingency table.

Table 2. Contingency table for co-occurrences of genes A and B

	Gene A present	Gene A absent	Total
Gene B present	8	2	10
Gene B absent	2	18	20
Total	10	20	30

Table 2 presents co-occurrence data for gene A and gene B in a total of 30 libraries. Both gene A and gene B occur 10 times in the libraries. Table 2 summarizes and presents 1) the number of times gene A and B are both present in a library, 2) the number of times gene A and B are both absent in a library, 3) the number of times gene A is present while gene B is absent, and 4) the number of times gene B is present while gene A is absent. The upper left entry is the number of times the two genes co-occur in a library, and the middle right entry is the number of times neither gene occurs in a library. The off diagonal entries are the number of times one gene occurs while the other does not. Both A and B are present eight times and absent 18 times, gene A is present while gene B is absent two times, and gene B is present while gene A is absent two times. The probability ("p-value") that the above association occurs due to chance as calculated using a Fisher exact test is 0.0003. Associations are generally considered significant if a p-value is less than 0.01 (Agresti, supra; Rice, supra).

This method of estimating the probability for coexpression of two genes makes several assumptions. The method assumes that the libraries are independent and are identically sampled. However, in practical situations, the selected cDNA libraries are not entirely independent because more than one library may be obtained from a single patient or tissue, and they are not entirely

identically sampled because different numbers of cDNA's may be sequenced from each library (typically ranging from 5,000 to 10,000 cDNA's per library). In addition, because a Fisher exact coexpression probability is calculated for each gene versus 41,419 other genes, a Bonferroni correction for multiple statistical tests is necessary.

Using the method of the present invention, we have identified 11 novel genes that exhibit strong association, or coexpression, with known genes that are inflammation-specific. These known inflammation genes include CD16, L-selectin, Src-like adapter protein (SLAP), IP-30, superoxidase homoenzyme subunits (p67phox, p47phox, and p40phox), alpha-1-antitrypsin (AAT), Clq-A, 5-lipoxygenase activating protein (FLAP), and SRC family tyrosine kinase (HCK). The results presented in Table 5 show that the expression of the 11 novel genes have direct or indirect association with the expression of known inflammation genes. Therefore, the novel genes can potentially be used in diagnosis, treatment, prognosis, or prevention of diseases associated with inflammation, or in the evaluation of therapies for diseases associated with inflammation. Further, the gene products of the 11 novel genes are potential therapeutic proteins and targets of therapeutics against diseases associated with inflammation.

Therefore, in one embodiment, the present invention encompasses a polynucleotide sequence comprising the sequence of SEQ ID Nos:1-11. These 11 polynucleotides are shown by the method of the present invention to have strong coexpression association with known inflammation genes and with each other. The invention also encompasses a variant of the polynucleotide sequence, its complement, or 18 consecutive nucleotides of a sequence provided in the above described sequences. Variant polynucleotide sequences typically have at least about 70%, more preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to NSEQ. One preferred method for identifying variants entails using NSEQ and/or PSEQ sequences to search against the GenBank primate (pri), rodent (rod), and mammalian (mam), vertebrate (vrtp), and eukaryote (eukp) databases, SwissProt, BLOCKS (Bairoch et al. (1997) Nucleic Acids Res 25:217-221), PFAM, and other databases that contain previously identified and annotated motifs, sequences, and gene functions. Methods that search for primary sequence patterns with secondary structure gap penalties (Smith (1992) Prot Eng 5:35-51) as well as algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul (1993) J Mol Evol 36:290-300; and Altschul et al. (1990) J Mol Biol 215:403-410), BLOCKS (Henikoff and Henikoff (1991) Nucleic Acids Res 19:6565-6572), Hidden Markov Models (HMM; Eddy (1996) Cur Opin Str Biol 6:361-365; and Sonnhammer et al. (1997) Proteins 28:405-420), and the like, can be used to manipulate and analyze nucleotide and amino acid sequences. These databases, algorithms and other methods are well known in the art and are described in Ausubel et

al. (1997; Short Protocols in Molecular Biology, John Wiley & Sons, New York NY)and in Meyers (1995; Molecular Biology and Biotechnology, Wiley VCH. New York NY).

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to SEQ ID NOs:1-11, and fragments thereof under stringent conditions. Stringent conditions can be defined by salt concentration, temperature, and other chemicals and conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, or raising the hybridization temperature.

For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent or solvent, and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Additional variations on these conditions will be readily apparent to those skilled in the art (Wahl and Berger (1987) Methods Enzymol 152:399-407; Kimmel (1987) Methods Enzymol 152:507-511; Ausubel, supra; and Sambrook et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY).

NSEQ or the polynucleotide sequences encoding PSEQ can be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. (See, e.g., Dieffenbach and Dveksler (1995) PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview NY; Sarkar (1993) PCR Methods Applic 2:318-322; Triglia et al. (1988) Nucleic Acids Res 16:8186; Lagerstrom et al. (1991) PCR Methods Applic 1:111-119; and Parker et al. (1991) Nucleic Acids Res 19:3055-306). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto, CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 18 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

In another aspect of the invention, NSEQ or the polynucleotide sequences encoding PSEQ can be cloned in recombinant DNA molecules that direct expression of PSEQ or the polypeptides encoded by NSEQ, or structural or functional fragments thereof, in appropriate host cells. Due to

the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express the polypeptides of PSEQ or the polypeptides encoded by NSEQ. The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter the nucleotide sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In order to express a biologically active polypeptide encoded by NSEQ or the polynucleotide sequences encoding PSEQ, or derivatives thereof, may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and NSEQ or polynucleotide sequences encoding PSEQ. Methods which are well known to those skilled in the art may be used to construct expression vectors containing NSEQ or polynucleotide sequences encoding PSEQ and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra and Ausubel, supra.)

A variety of expression vector/host cell systems may be utilized to contain and express NSEQ or polynucleotide sequences encoding PSEQ. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (baculovirus); plant cell systems transformed with viral expression vectors, cauliflower mosaic virus (CaMV) or tobacco mosaic virus (TMV), or with bacterial expression vectors (Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed. For long term production of recombinant proteins in mammalian systems, stable expression of a polypeptide encoded by NSEQ in cell lines is preferred. For example, NSEQ or sequences encoding PSEQ can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector.

In general, host cells that contain NSEQ and that express PSEQ may be identified by a

variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences. Immunological methods for detecting and measuring the expression of PSEQ using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS).

Host cells transformed with NSEQ or polynucleotide sequences encoding PSEQ may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of NSEQ or polynucleotides encoding PSEQ may be designed to contain signal sequences which direct secretion of PSEQ through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC, Manassas, MD) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant NSEQ or nucleic acid sequences encoding PSEQ are ligated to a heterologous sequence resulting in translation of a fusion protein containing heterologous protein moieties in any of the aforementioned host systems. Such heterologous protein moieties facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, hemagglutinin (HA) and monoclonal antibody epitopes.

In another embodiment, NSEQ or sequences encoding PSEQ are synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers et al. (1980) Nucleic

Acids Symp Ser (7)215-223; Horn et al. (1980) Nucleic Acids Symp Ser (7)225-232; and Ausubel, supra). Alternatively, PSEQ or a polypeptide sequence encoded by NSEQ itself, or a fragment thereof, may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge et al. (1995) Science 269:202-204). Automated synthesis may be achieved using the ABI 431A Peptide synthesizer (PE Biosystems, Foster City CA). Additionally, PSEQ or the amino acid sequence encoded by NSEQ, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a polypeptide variant.

In another embodiment, the invention entails a substantially purified polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NOs:12-17 or fragments thereof.

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The sequences of the these genes can be used in diagnosis, prognosis, treatment, prevention, and evaluation of therapies for diseases associated with inflammation, particularly disorders such as rheumatoid arthritis, Crohn's disease, multiple sclerosis, asthma, and allergy.

In one preferred embodiment, the polynucleotide sequences of NSEQ or the polynucleotides encoding PSEQ are used for diagnostic purposes to determine the absence, presence, and excess expression of PSEQ. The polynucleotides may be at least 18 nucleotides long, complementary RNA and DNA molecules, branched nucleic acids, and peptide nucleic acids (PNAs). Alternatively, the polynucleotides are used to detect and quantitate gene expression in samples in which expression of NSEQ or the polypeptides encoded by NSEQ are correlated with disease. Additionally, NSEQ or the polynucleotides encoding PSEQ can be used to detect genetic polymorphisms associated with a disease. These polymorphisms may be detected at the transcript cDNA or genomic level.

The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding PSEQ, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 70% sequence identity to any of the NSEQ or PSEQ-encoding sequences.

Means for producing specific hybridization probes for DNAs encoding PSEQ include the cloning of NSEQ or polynucleotide sequences encoding PSEQ into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to

synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, by fluorescent labels, and the like. The polynucleotide sequences encoding PSEQ may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; and in microarrays utilizing fluids or tissues from patients to detect altered PSEQ expression. Such qualitative or quantitative methods are well known in the art.

NSEQ or the nucleotide sequences encoding PSEQ can be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed, and the signal is quantitated and compared with a standard value, typically, derived from a non-diseased sample. If the amount of signal in the patient sample is altered in comparison to the standard value then the presence of altered levels of nucleotide sequences of NSEQ or those encoding PSEQ in the sample indicates the presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

Once the presence of a disease is established and a treatment protocol is initiated, hybridization or amplification assays can be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in a healthy subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

The polynucleotides may be used for the diagnosis of a variety of diseases associated with inflammation, particularly for diseases including, but not limited to, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyenodocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus,

systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma.

The polynucleotides may also be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify splice variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disease, to diagnose a disease, and to develop and monitor the activities of therapeutic agents.

In yet another alternative, polynucleotides may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich et al. (1995) In: Meyers, supra). Microarrays may be used to detect genetic diversity at the genome level.

In another embodiment, antibodies which specifically bind PSEQ may be used for the diagnosis of diseases characterized by the over-or-underexpression of PSEQ or polypeptides encoded by NSEQ. A variety of protocols for measuring PSEQ, or the polypeptides encoded by NSEQ, including ELISAs, RIAs, and FACS are well known in the art and provide a basis for diagnosing altered or abnormal levels of the expression of PSEQ or the polypeptides encoded by NSEQ. Standard values for PSEQ expression are established by combining body fluids or cell extracts taken from healthy subjects, preferably human, with antibody to PSEQ or a polypeptide encoded by NSEQ under conditions suitable for complex formation. The amount of complex formation may be quantitated by various methods, preferably by photometric means. Quantities of PSEQ or the polypeptides encoded by NSEQ expressed in disease samples from, for example, biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing or monitoring disease. Alternatively, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PSEQ or the polypeptides encoded by NSEQ specifically compete with a test compound for binding the polypeptides. Antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PSEQ or the polypeptides encoded by NSEQ.

In another aspect, the polynucleotides and polypeptides of the present invention can be employed for treatment or the monitoring of therapeutic treatments for cancers. The polynucleotides of NSEQ or those encoding PSEQ, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotides of NSEQ or those encoding PSEQ may be used in situations in which it would be desirable to block the

transcription or translation of the mRNA.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding PSEQ. (See, e.g., Sambrook, supra; and Ausubel, supra.)

Genes having polynucleotide sequences of NSEQ or those encoding PSEQ can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or a fragment thereof, encoding PSEQ. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee et al. (1994) In: Huber and Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.)

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the cleavage of mRNA and decrease the levels of particular mRNAs, such as those comprising the polynucleotide sequences of the invention. (See, e.g. Rossi, (1994) Current Biology 4:469-471.) Ribozymes may cleave mRNA at specific cleavage sutes. Alternatively, ribozymes may cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The construction and production of ribozymes is well known in the art and is described in Meyers (supra).

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiester linkages within the backbone of the molecule. Alternatively, nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases may be included.

Alternatively, the polynucleotides of the invention may be integrated into a genome by somatic or germ cell gene therapy. Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors

may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman et al. (1997) Nature Biotechnol 15:462-466.)

Additionally, endogenous polynucleotide expression may be inactivated using homologous recombination methods which insert an inactive gene sequence at the target sequence location. (See, e.g. Thomas and Capecchi (1987) Cell 51:503-512.)

Further, an antagonist or antibody of a polypeptide of PSEQ or encoded by NSEQ may be administered to a subject to treat or prevent a cancer associated with increased expression or activity of PSEQ. An antibody which specifically binds the polypeptide may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express the the polypeptide.

Antibodies to PSEQ may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies, those which inhibit dimer formation, are especially preferred for therapeutic use. Monoclonal antibodies to PSEQ may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. In addition, techniques developed for the production of chimeric antibodies can be used. (See, e.g., Meyers, supra.) Alternatively, techniques described for the production of single chain antibodies may be employed. Antibody fragments which contain specific binding sites for PSEQ or the polypeptide sequences encoded by NSEQ may also be generated.

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art.

Yet further, an agonist of PSEQ or that encoded by NSEQ may be administered to a subject to treat or prevent a cancer associated with decreased expression or activity of the polypeptide.

An additional aspect of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of

polypeptides of PSEQ or those encoded by NSEQ, antibodies to the polypeptides, and mimetics, agonists, antagonists, or inhibitors of the polypeptides. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example, polypeptides of PSEQ or those encoded by NSEQ, or fragments thereof, antibodies of the polypeptides, and agonists, antagonists or inhibitors of the polypeptides, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics.

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

EXAMPLES

It is understood that this invention is not limited to the particular methodology, protocols, and reagents described, as these may vary. It is also understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to limit the scope

of the present invention which will be limited only by the appended claims. The examples below are provide to illustrate the subject invention and are not included for the purpose of limiting the invention.

I cDNA Library Construction

The cDNA library, OVARTUT05, was selected as an example to demonstrate the construction of the cDNA libraries from which the sequences used to identify genes associated with inflammation were derived. The OVARTUT05 library was constructed from tumorous ovary tissue obtained from a 62 year-old Caucasian female. Pathology indicated a grade 4 endometrioid carcinoma with extensive squamous differentiation forming a solid mass in the right ovary. The cervix showed mild chronic cervicitis, and the posterior uterine serosa showed focal endometriosis. Prior pathology indicated weakly proliferative endometrium with excessive stromal breakdown in the uterus and a mild chronic cervicitis with prominent nabothian cyst in the cervix.

The frozen tissue was homogenized and lysed using a POLYTRON homogenizer (PT-3000; Brinkmann Instruments, Westbury NY) in guanidinium isothiocyanate solution. The lysate was centrifuged over a 5.7 M CsCl cushion using an SW28 rotor in a L8-70M ultracentrifuge (Beckman Coulter, Fullerton CA) for 18 hours at 25,000 rpm at ambient temperature. The RNA was extracted with acid phenol, pH 4.7, precipitated using 0.3 M sodium acetate and 2.5 volumes of ethanol, resuspended in RNAse-free water, and treated iwth DNase at 37°C. The RNA extraction was repeated with acid phenol, pH 4.7 and precipitated with sodium acetate and ethanol as before. The mRNA was then isolated using the OLIGOTEX kit (Qiagen, Chatsworth CA) and used to construct the cDNA library.

The mRNA was handled according to the recommended protocols in the SUPERSCRIPT Plasmid system (Life Technologies, Rockville MD). The cDNAs were fractionated on a SEPHAROSE CL4B column (Amersham Pharmacia Biotech, Piscataway NJ), and those cDNAs exceeding 400 bp were ligated into pINCY 1 plasmid (Incyte Pharmaceuticals, Palo Alto CA). The plasmid was subsequently transformed into DH5α competent cells (Life Technologies).

II Isolation and Sequencing of cDNA Clones

Plasmid DNA was released from the cells and purified using the REAL Prep 96 Plasmid kit (Qiagen). This kit enabled the simultaneous purification of 96 samples in a 96-well block using multi-channel reagent dispensers. The recommended protocol was employed except for the following changes: 1) the bacteria were cultured in 1 ml of sterile Terrific Broth (Life Technologies) with carbenicillin at 25 mg/L and glycerol at 0.4%; 2) after inoculation, the cultures were incubated for 19 hours and at the end of incubation, the cells were lysed with 0.3 ml of lysis

buffer: and 3) following isopropanol precipitation, the plasmid DNA pellet was resuspended in 0.1 ml of distilled water. After the last step in the protocol, samples were transferred to a 96-well block for storage at 4° C.

The cDNAs were prepared using a MICROLAB 2200 (Hamilton, Reno NV) in combination with DNA ENGINE thermal cyclers (PTC200; MJ Research, Watertown MA) and sequenced by the method of Sanger et al. (1975, J Mol Biol 94:441f) using ABI PRISM 377 DNA Sequencing systems (PE Biosystems).

III Selection, Assembly, and Characterization of Sequences

The sequences used for coexpression analysis were assembled from EST sequences, 5' and 3' longread sequences, and full length coding sequences. Selected assembled sequences were expressed in at least three cDNA libraries.

The assembly process is described as follows. EST sequence chromatograms were processed and verified. Quality scores were obtained using PHRED (Ewing et al. (1998) Genome Res 8:175-185; Ewing and Green (1998) Genome Res 8:186-194). Then the edited sequences were loaded into a relational database management system (RDBMS). The EST sequences were clustered into an initial set of bins using BLAST with a product score of 50. All clusters of two or more sequences were created as bins. The overlapping sequences represented in a bin correspond to the sequence of a transcribed gene.

Assembly of the component sequences within each bin was performed using a modification of PHRAP, a publicly available program for assembling DNA fragments (Green, University of Washington, Seattle WA). Bins that showed 82% identity from a local pair-wise alignment between any of the consensus sequences were merged.

Bins were annotated by screening the consensus sequence in each bin against public databases, such as GBpri and GenPept from NCBI. The annotation process involved a FASTn screen against the GBpri database in GenBank. Those hits with a percent identity of greater than or equal to 70% and an alignment length of greater than or equal to 100 base pairs were recorded as homolog hits. The residual unannotated sequences were screened by FASTx against GenPept. Those hits with an E value of less than or equal to 10^{-8} are recorded as homolog hits.

Sequences were then reclustered using BLASTn and Cross-Match, a program for rapid protein and nucleic acid sequence comparison and database search (Green, supra), sequentially. Any BLAST alignment between a sequence and a consensus sequence with a score greater than 150 was realigned using cross-match. The sequence was added to the bin whose consensus sequence gave the highest Smith-Waterman score amongst local alignments with at least 82% identity. Non-matching sequences created new bins. The assembly and consensus generation

processes were performed for the new bins.

IV Coexpression Analyses of Known Inflammation Genes

Known inflammation genes were selected to identify novel genes that are closely associated with inflammation. These known genes were CD16, L-selectin, Src-like adapter protein (SLAP), IP-30, superoxidase homoenzyme subunits (p67phox, p47phox, and p40phox), alpha-1-antitrypsin (AAT), Clq-A, 5-lipoxygenase activating protein (FLAP), and SRC family tyrosine kinase (HCK).

The known inflammation genes that we examined in this analysis, and brief descriptions of their functions, are listed in Table 4.

Table 4. Known Inflammation Genes.

Gene	Description & references
CD16	receptor for IgG a.k.a. FcgammaRIII Phagocytosis of complement-generated immune complexes occurs through CD16 (Tamm et al. (1996) J Biol Chem 271:3659-66; Marsh et al. (1998) J Immunol 160:3942-8)
L-selectin	Leukocyte adhesion molecule Binds carbohydrate ligand on endothelial cell glycoprotein Adhesion is required for extravasation near inflammation site; auxiliary function in neutrophil activation during inflammation (Frohlich et al. (1998) Blood 91:2558-64; Girard and Amalric (1998) Adv Exp Med Biol 435:55-62)
SLAP	Src-like adapter protein Associated with Eck RPTK transduction pathway; Eck RPTK autocrine loop implicated in inflammation (Pandey, et al. (1995) J Biol Chem 270:19201-4; Pandey et al. (1995) Science 268:567-9)
IP-30	Functions in MHC Class II processing of peptides; implicated in inflammation, α-interferon inducible (Luster et al. (1988) J Biol Chem 263:12036-43; Arunachalam et al. (1998) J Immunol 160:5797-806; Schuelke et al. (1998) Biochem Biophys Res Commun 245:599-606)
p67phox, p47phox, p40phox	superoxidase holoenzyme subunits Macrophages utilize reactive superoxide in degradation of phagocytosed matter, induced by complement (Ratnam and Mookerjea (1998) Immunology 94:560-568)
AAT	alpha-1-antitrypsin (AAT) inhibits trypsin, a protease

		Differentially expressed in inflammation, several alleles linked to chronic inflammatory disorders (Breit and Penny (1980) Aust NZJ Med 10:449-53; Takeuchi, Kobayashi et al. (1984) Int J Tissue React 6:1-8)
	C1q-A	First complement component, subcomponent q, subunit A (Alberts et al. (1994) Molecular Biology of the Cell, Garland Publishing, New York NY, p. 1214)
	FLAP	5-lipoxygenase activating protein Lipoxygenase enzyme catalyzes formation of leukotrienes which are potent inflammatory mediators, FLAP is an anti-inflammatory therapeutic target (Byrum et al. (1997) J Exp Med 185:1065-75; Muller-Peddinghaus (1997) J Physiol Pharmacol 48:529-36)
	HCK	Src-family tyrosine kinase specific to hematopoietic cells Functions in integrin signaling, mouse knockouts have impaired inflammation response (Lowell and Berton (1998) Proc Natl Acad Sci 95:7580-4)

The coexpression of the 11 known genes with each other is shown in Table 5. The entries in Table 5 are the negative log of the p-value (- log p) for the coexpression of the two genes. As shown, the method successfully identified the strong association of the known genes among themselves, indicating that the coexpression analysis method of the present invention was effective in identifying genes that are closely associated with inflammation.

We have also identified 11 novel genes that show strong association with known inflammation genes from a total of 41,419 assembled gene sequences. The degree of association was measured by probability values and has a cutoff of p value less than 0.00001. This was followed by annotation and literature searches to insure that the genes that passed the probability test have strong association with known inflammation genes. This process was reiterated so that the initial 41,419 genes were reduced to the final 11 inflammation-associated genes. Details of the expression patterns for the 11 novel inflammation genes are presented in Table 5.

Each of the 11 novel genes is coexpressed with at least one of the known genes with a p-value of less than 10E-05. The coexpression of the 11 novel genes with the known genes are shown in Table 5. The entries in Table 5 are the negative log of the p-value (- log p) for the coexpression of the two genes. The novel genes identified are listed in the table by their Incyte clone numbers, and the known genes their abbreviated names as shown in Ex.5. V

Table 5. Coexpression analysis of novel genes with known inflammation genes(- log p).

	CD16	L-selectin	SLAP	IP-30	p67-phox	AAT	p47-phox	C1qA	p40-phox	FLAP	HCK	1221361	3055142	402234	3507924	1335016	3054032	569989	2349263	2471716	2726173	706377
CD16																						
L-selectin	4																					
SLAP	5	6																				
IP-30	5	3	4																			
P67-phox	3	5	7	1																		
AAT	6	2	4	1	5																	
P47-phox	5	6	5	1.	7	3																
C1qA	7	2	6	1	3	7	6															
P40-phox	5	5	3	4	7	4	6	1														
FLAP	7	5	3	1	5	3	5	7	3													
HCK	9	8	4	5	8	5	7	3	6	3												
1221361	3	5	7	4	3	1	4	2	4	2	4											
3055142	6	5	9	4	5	3	8	1	4	3	8	4										
402234	3	6	4	4	2	0	6	1	3	4	2	3	1									
3507924	2	5	3	4	4	8	4	1	7	3	2	3	2	4								
1335016	7	3	3	8	2	2	5	6	3	4	3	4	5	2	2							
3054032	5	11	9	5	4	4	7	7	7	8	7	5	7	5	4	4						
569989	4	4	4	6	9	1	8	2	4	5	4	4	4	7	2	2	5					
2349263	8	1	2	6	4	4	3	8	5	5	6	3	3	1	3	9	5	4				
2471716	3	5	3	7	5	1	7	4	5	2	4	3	5	4	5	4	8	3	7			
2726173	3	8	5	4	6	2	7	0	2	3	5	4	3	4	4	2	3	3	2	5		
706377	4	5	5	8	6	5	10	3	6	3	3	4	4	9	4	5	5	7	3	6	3	

V Novel Genes Associated with Inflammation

Eleven novel genes were identified from the data shown in Table 5 to be associated with inflammation.

Nucleic acids comprising the consensus sequences of SEQ ID NOs:1-11 of the present invention were first identified from Incyte Clones 402234, 569989, 706377, 1221361, 1335016, 2349263, 2471716, 2726173, 3054032, 3055142, and 3507924, respectively, and assembled according to Example III. BLAST and other motif searches were performed for SEQ ID NOs:1-11 according to Example VII. The sequences of SEQ ID NOs:1-11 were translated and sequence identity was sought with known sequences. Amino acids comprising the consensus sequences of SEQ ID NOs:12, 13, 14, 15, 16, and 17 of the present invention were encoded by the nucleic acids of SEQ ID NOs:1, 2, 6, 7, 8, and 11, respectively. SEQ ID NOs:12-17 were also analyzed using BLAST and other motif search tools as disclosed in Example VII.

SEQ ID NO:3 is 1229 nucleic acids in length and has about 99% match from about nucleic acid 250 to about nucleic acid 1216 with a human basement membrane-induced gene identified in

a human endometrial adenocarcinoma cell line (g3132521). SEQ ID NO:4 is about 1261 nucleic acids in length and has about 34% sequence identity from nucleic acid 23 to nucleic acid 994 with a predicted sequence similar to a RNA recognition motif (g2645068). SEQ ID NO:5 is 1340 nucleic acids in length and has about 60% sequence identity from about nucleic acid 21 to about nucleic acid 925 with a human prostaglandin transporter hPGT mRNA (g3006201). The amino acid sequence encoded by SEQ ID NO:5 also exhibits several potential transmembrane domains as identified by HMM analysis. SEQ ID NO:9 is 2309 nucleic acids in length and shows similarity from about nucleic acid 104 to about nucleic acid 785 with a human polycystic kidney disease-associated protein gene (g790818).

SEQ ID NO:12 is 127 amino acid residues in length and shows about 50% sequence identity from about residue 37 to about residue 106 with a tobacco LIM-domain-containing protein (g1841464). The LIM domain is a cysteine-rich, zinc-binding motif of about 60 amino-acid residues that plays a potential role in DNA binding and regulation (Perez-Alvarado et al. (1994) Nat Struct Biol 1: 388-398). PFAM analysis shows that residues 40 to 97 of SEQ ID NO:12 encompasses the LIM domain. SEQ ID NO:13 is 93 amino acids in length and has a potential signal peptide sequence encompassing residues 1-18. SEQ ID NO:13 also exhibits a potential transmembrane domain encompassing residues 47 to 69. SEQ ID NO:14 is 225 amino acids in length and has about 32% sequence identity from about residue 5 to about residue 135 with a mouse high affinity IgE receptor beta subunit (g309225). SEQ ID NO:15 is 547 amino acid residues in length and has about 35% sequence identity from about residue 413 to about 546 with a rat beta-chimaerin, a GTPase-activating protein expressed exclusively in the testis at the onset of sexual maturation (g203117). PFAM analysis shows that SEQ ID NO:15 has sequence homology from about residue 353 to about residue 523 with the GTPase-activator protein for Rho-like GTPases. SEQ ID NO:16 is 265 amino acids in length and shows about 93% sequence identity from about residue 39 to about residues 265 with Maxp1, a rat protein which interacts with Mss4, a guanine nucleotide exchange factor (g2459833), and about 91% sequence identity from about residue 38 to about residue 265 with Nore1, a mouse putative Ras effector that plays an essential role in transmitting growth and differentiation signals received from Ras proteins(g2997698). This is confirmed by PFAM analysis that shows that SEQ ID NO:16 from about residue 119 to about residue 211 matches a Ras association domain which interacts directly with the Ras proteins. SEQ ID NO:17 is 394 amino acids in length and exhibits a potential signal peptide sequence encompassing residues 1 to 19 and a potential transmembrane domain encompassing residues 273 to 295.

VI Homology Searching for Inflammation Genes and the Proteins

Polynucleotide sequences, SEQ ID NOs:1-11, and polypeptide sequences, SEQ ID NOs:12-17, were queried against databases derived from sources such as GenBank and SwissProt. These databases, which contain previously identified and annotated sequences, were searched for regions of similarity using BLAST (Altschul, supra) and Smith-Waterman alignment (Smith, supra). BLAST searched for matches and reported only those that satisfied the probability thresholds of 10^{-25} or less for nucleotide sequences and 10^{-8} or less for polypeptide sequences.

The polypeptide sequences were also analyzed for known motif patterns using MOTIFS, SPSCAN, BLIMPS, and Hidden Markov Model (HMM)-based protocols. MOTIFS (Genetics Computer Group, Madison WI) searches polypeptide sequences for patterns that match those defined in the Prosite Dictionary of Protein Sites and Patterns (Bairoch et al. supra), and displays the patterns found and their corresponding literature abstracts. SPSCAN (Genetics Computer Group) searches for potential signal peptide sequences using a weighted matrix method (Nielsen et al. (1997) Prot Eng 10:1-6). Hits with a score of 5 or greater were considered. BLIMPS uses a weighted matrix analysis algorithm to search for sequence similarity between the polypeptide sequences and those contained in BLOCKS, a database consisting of short amino acid segments, or blocks, of 3-60 amino acids in length, compiled from the PROSITE database (Henikoff and Henikoff, supra; Bairoch et al. supra), and those in PRINTS, a protein fingerprint database based on non-redundant sequences obtained from sources such as SwissProt, GenBank, PIR, and NRL-3D (Attwood et al. (1997) J Chem Inf Comput Sci 37:417-424). For the purposes of the present invention, the BLIMPS searches reported matches with a cutoff score of 1000 or greater and a cutoff probability value of 1.0×10^{-3}. HMM-based protocols were based on a probabilistic approach and searched for consensus primary structures of gene families in the protein sequences (Eddy, supra; Sonnhammer et al. supra). More than 500 known protein families with cutoff scores ranging from 10 to 50 bits were selected for use in this invention.

VII Labeling and Use of Individual Hybridization Probes

Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μCi of [γ-^{32}P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (NEN Life Science Products, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine resin column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba 1, or Pvu II (NEN Life Science Products).

The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to

NYTRANPLUS membranes (Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR film (Eastman Kodak. Rochester NY) is exposed to the blots for several hours, hybridization patterns are compared.

VIII Production of Specific Antibodies

Any of the SEQ ID NOs:12-17, or fragments thereof, substantially purified using polyacrylamide gel electrophoresis (Harrington (1990) Methods Enzymol 182:488-495) or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the amino acid sequence is analyzed using LASERGENE software (DNASTAR, Madison WI) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A Peptide synthesizer (PE Biosystems) using Fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester to increase immunogenicity. Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, by binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

What is claimed is:

1. A substantially purified polynucleotide comprising a gene that is coexpressed with one or more known inflammation genes in a plurality of biological samples, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase.

2. The polynucleotide of claim 1, comprising a polynucleotide sequence selected from:

(a) a polynucleotide sequence selected from the group consisting of SEQ ID NOs:1- 11;

(b) a polynucleotide sequence selected from the group consisting of SEQ ID NOs:12-17;

(c) a polynucleotide sequence having at least 70% identity to the polynucleotide sequence of (a) or (b);

(d) a polynucleotide sequence which is complementary to the polynucleotide sequence of (a), (b), or (c);

(e) a polynucleotide sequence comprising at least 18 sequential nucleotides of the polynucleotide sequence of (a),(b), (c), or (d); and

(f) a polynucleotide which hybridizes under stringent conditions to the polynucleotide of (a),(b),(c), (d) or (e).

3. A substantially purified polypeptide comprising the gene product of a gene that is coexpressed with one or more known inflammation genes in a plurality of biological samples, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase.

4. The polypeptide of claim 3, comprising a polypeptide sequence selected from the group consisting of:

(a) the polypeptide sequence selected from the group consisting of SEQ ID NOs:12-17;

(b) a polypeptide sequence having at least 85% identity to the polypeptide sequence of (a); and

(c) a polypeptide sequence comprising at least 6 sequential amino acids of the polypeptide sequence of (a) or (b).

5. An expression vector comprising the polynucleotide of claim 2.

6. A host cell comprising the expression vector of claim 5.

7. A pharmaceutical composition comprising the polynucleotide of claim 2 or the polypeptide of claim 3 in conjunction with a suitable pharmaceutical carrier.

8. An antibody which specifically binds to the polypeptide of claim 4.

9. A method for diagnosing a disease or condition associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase, the method comprising the steps of:

(a) providing a sample comprising one of more of said coexpressed genes;

(b) hybridizing the polynucleotide of claim 2 to said coexpressed genes under conditions effective to form one or more hybridization complexes;

(c) detecting the hybridization complexes; and

(d) comparing the levels of the hybridization complexes with the level of hybridization complexes in a non-diseased sample, wherein the altered level of hybridization complexes compared with the level of hybridization complexes of a nondiseased sample correlates with the presence of the disease or condition.

10. A method for treating or preventing a disease associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes in a subject in need, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase, the method comprising the step of administering to said subject in need the pharmaceutical composition of claim 7 in an amount effective for treating or preventing said disease.

11. A method for treating or preventing a disease associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes in a subject in need, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase, the method comprising the step of administering to said subject in need the antibody of claim 8 in an amount effective for treating or preventing said disease.

12. A method for treating or preventing a disease associated with the altered expression of a gene that is coexpressed with one or more known inflammation genes in a subject in need, wherein each known inflammation gene is selected from the group consisting of CD16, L-selectin, Src-like adapter protein, IP-30, superoxidase homoenzyme subunits, alpha-1-antitrypsin, Clq-A, 5-lipoxygenase activating protein, and SRC family tyrosine kinase, the method comprising the step of administering to said subject in need the polynucleotide sequence of claim 2 in an amount

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<211> 3144
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No.: 2726173CB1

<400> 8

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<210> 9
<211> 2309
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No.: 3054032CB1

<400> 9

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<211> 1666
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No.: 3055142CB1

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<211> 1751
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No.: 3507924CB1

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<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
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Ser Leu Arg Ala Gln Val Lys Glu Thr Cys Ala Ala Cys Gln Lys
35 40 45
Thr Val Tyr Pro Met Glu Arg Leu Val Ala Asp Lys Leu Ile Phe
50 55 60
His Asn Ser Cys Phe Cys Cys Lys His Cys His Thr Lys Leu Ser
65 70 75
Leu Gly Ser Tyr Ala Ala Leu His Gly Glu Phe Tyr Cys Lys Pro
80 85 90
His Phe Gln Gln Leu Phe Lys Ser Lys Gly Asn Tyr Asp Glu Gly
95 100 105
Phe Gly Arg Lys Gln His Lys Glu Leu Trp Ala His Lys Glu Val
110 115 120
Asp Pro Gly Thr Lys Thr Ala
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<210> 13
<211> 93
<212> PRT
<213> Homo sapiens

<220>
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<400> 13
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Phe Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu
                 35                  40                  45
Ser Leu Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala
                 50                  55                  60
Ser Leu Leu Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg
                 65                  70                  75
Arg Ser Pro Ala Gln Glu Asp Gly Lys Val Tyr Ile Asn Met Pro
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Gly Arg Gly
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<212> PRT
<213> Homo sapiens

<220>
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<223> Incyte ID No.: 2349263CD1

<400> 14
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Asn Gln Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile
                 35                  40                  45
Lys Val Ile Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu
                 50                  55                  60
Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe
                 65                  70                  75
Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile
                 80                  85                  90
Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala Thr
                 95                 100                 105
Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly
                110                 115                 120
Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu
                125                 130                 135
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu
                140                 145                 150
Leu Asp Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe
                155                 160                 165
Tyr His Asp Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala
                170                 175                 180
Ser Leu Ala Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu
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185 190 195
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200 205 210
Ala Tyr Ser Asp Phe Pro Gly Val Ser Val Leu Ala Gly Phe Thr
215 220 225

<210> 15
<211> 547
<212> PRT
<213> Homo sapiens

<220>
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35 40 45
Cys Phe Tyr Ile Asn Ser Leu Thr Gly Cys Lys Ser Trp Lys Pro
50 55 60
Pro Arg Arg Ser Arg Ser Glu Thr Asn Pro Gly Ser Met Glu Gly
65 70 75
Thr Gln Thr Leu Lys Arg Asn Asn Asp Val Leu Gln Pro Gln Ala
80 85 90
Lys Gly Phe Arg Ser Asp Thr Gly Thr Pro Glu Pro Leu Asp Pro
95 100 105
Gln Gly Ser Leu Ser Leu Ser Gln Arg Thr Ser Gln Leu Asp Pro
110 115 120
Pro Ala Leu Gln Ala Pro Arg Pro Leu Pro Gln Leu Leu Asp Asp
125 130 135
Pro His Glu Val Glu Lys Ser Gly Leu Leu Asn Met Thr Lys Ile
140 145 150
Ala Gln Gly Gly Arg Lys Leu Arg Lys Asn Trp Gly Pro Ser Trp
155 160 165
Val Val Leu Thr Gly Asn Ser Leu Val Phe Tyr Arg Glu Pro Pro
170 175 180
Pro Thr Ala Pro Ser Ser Gly Trp Gly Pro Ala Gly Ser Arg Pro
185 190 195
Glu Ser Ser Val Asp Leu Arg Gly Ala Ala Leu Ala His Gly Arg
200 205 210
His Leu Ser Ser Arg Arg Asn Val Leu His Ile Arg Thr Ile Pro
215 220 225
Gly His Glu Phe Leu Leu Gln Ser Asp His Glu Thr Glu Leu Arg
230 235 240
Ala Trp His Arg Ala Leu Arg Thr Val Ile Glu Arg Leu Asp Arg
245 250 255
Glu Asn Pro Leu Glu Leu Arg Leu Ser Gly Ser Gly Pro Ala Glu
260 265 270
Leu Ser Ala Gly Glu Asp Glu Glu Glu Glu Ser Glu Leu Val Ser
275 280 285
Lys Pro Leu Leu Arg Leu Ser Ser Arg Arg Ser Ser Ile Arg Gly
290 295 300
Pro Glu Gly Thr Glu Gln Asn Arg Val Arg Asn Lys Leu Lys Arg
305 310 315
Leu Ile Ala Lys Arg Pro Pro Leu Gln Ser Leu Gln Glu Arg Gly
320 325 330
Leu Leu Arg Asp Gln Val Phe Gly Cys Gln Leu Glu Ser Leu Cys
335 340 345

Gln Arg Glu Gly Asp Thr Val Pro Ser Phe Leu Arg Leu Cys Ile
350 355 360
Ala Ala Val Asp Lys Arg Gly Leu Asp Val Asp Gly Ile Tyr Arg
365 370 375
Val Ser Gly Asn Leu Ala Val Val Gln Lys Leu Arg Phe Leu Val
380 385 390
Asp Arg Glu Arg Ala Val Thr Ser Asp Gly Arg Tyr Val Phe Pro
395 400 405
Glu Gln Pro Gly Gln Glu Gly Arg Leu Asp Leu Asp Ser Thr Glu
410 415 420
Trp Asp Asp Ile His Val Val Thr Gly Ala Leu Lys Leu Phe Leu
425 430 435
Arg Glu Leu Pro Gln Pro Leu Val Pro Pro Leu Leu Leu Pro His
440 445 450
Phe Arg Ala Ala Leu Ala Leu Ser Glu Ser Glu Gln Cys Leu Ser
455 460 465
Gln Ile Gln Glu Leu Ile Gly Ser Met Pro Lys Pro Asn His Asp
470 475 480
Thr Leu Arg Tyr Leu Leu Glu His Leu Cys Arg Val Ile Ala His
485 490 495
Ser Asp Lys Asn Arg Met Thr Pro His Asn Leu Gly Ile Val Phe
500 505 510
Gly Pro Thr Leu Phe Arg Pro Glu Gln Glu Thr Ser Asp Pro Ala
515 520 525
Ala His Ala Leu Tyr Pro Gly Gln Leu Val Gln Leu Met Leu Thr
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Asn Phe Thr Ser Leu Phe Pro
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<210> 16
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No.: 2726173CD1

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Leu Lys Leu Arg Arg Pro Val Thr Val Pro Ala Gly Ile Arg Pro
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Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn Leu Ala Ala Thr
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Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp Ala Ile Lys
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Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val Ile Gln
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Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys Phe
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Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln

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35 40 45
Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser
50 55 60

Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser
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Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu
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Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp
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Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu
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Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
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Ile Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val
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Ile Val Phe Arg Tyr Tyr His Lys Leu Arg Met Ser Val Glu Tyr
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Ser Gln Ser Trp Gly His Phe Gln Asn Arg Val Asn Leu Val Gly
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Glu Ser Asp Gly Gly Asn Tyr Thr Cys Ser Ile His Leu Gly Asn
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Leu Val Phe Lys Lys Thr Ile Val Leu His Val Ser Pro Glu Glu
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